

WEST Search History

DATE: Thursday, July 06, 2006

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=AND</i>			
<input type="checkbox"/>	L11	l2 and l9	20
<input type="checkbox"/>	L10	l1 and L9	21
<input type="checkbox"/>	L9	l6 or l7 or L8	270
<input type="checkbox"/>	L8	edward.in. and thayer.in.	82
<input type="checkbox"/>	L7	philippa.in. and webster.in.	10
<input type="checkbox"/>	L6	james.in. and holloway.in.	186
<input type="checkbox"/>	L5	glycoprotein near hormone-1	3
<input type="checkbox"/>	L4	L2 and mammalian	17423
<input type="checkbox"/>	L3	l2 and mammalian	15
<input type="checkbox"/>	L2	l1 and hormone	25603
<input type="checkbox"/>	L1	glycoprotein	56365

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:18:28 ; Search time 200 Seconds
(without alignments)
297.191 Million cell updates/sec

Title: US-10-733-597-2

Perfect score: 722

Sequence: 1 MKLAFLFLGPMALLLLAGYG. VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
<hr/>						
1	722	100.0	130	4	AAG63211	Aag63211 Amino aci
2	722	100.0	130	4	AAG64064	Aag64064 Human ant
3	722	100.0	130	4	AAE09440	Aae09440 Human sbg
4	722	100.0	130	5	AAU97612	Aau97612 Human OGH
5	722	100.0	130	5	AAU96153	Aau96153 Human BRP
6	722	100.0	130	5	AAU10366	Aau10366 Human bet
7	722	100.0	130	6	ABG74206	Abg74206 Human gly

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:14:53 ; Search time 39.661 Seconds
(without alignments)
286.906 Million cell updates/sec

Title: US-10-733-597-2

Perfect score: 722

Sequence: 1 MKL AFLFLGPMALLL LAGYG. VAI RCD CGACSTATTECETI 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	521	72.2	118	3	US-10-162-335-26	Sequence 26, Appl
2	178	24.7	149	1	US-08-425-673-5	Sequence 5, Appl
3	178	24.7	203	2	US-09-059-625-88	Sequence 88, Appl
4	170	23.5	104	2	US-08-918-288-74	Sequence 74, Appl
5	170	23.5	104	2	US-09-282-357-74	Sequence 74, Appl
6	170	23.5	108	2	US-08-918-288-73	Sequence 73, Appl
7	170	23.5	108	2	US-09-282-357-73	Sequence 73, Appl
8	170	23.5	111	2	US-08-918-288-72	Sequence 72, Appl
9	170	23.5	111	2	US-09-282-357-72	Sequence 72, Appl
10	164.5	22.8	242	2	US-09-059-625-74	Sequence 74, Appl

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:18:48 ; Search time 72 Seconds
(without alignments)
836.360 Million cell updates/sec

Title: US-10-733-597-2

Perfect score: 722

Sequence: 1 MKL AFLFLGPMALLL LAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	722	100.0	130	3	US-09-818-954A-1	Sequence 1, Appli
2	722	100.0	130	3	US-09-943-388-2	Sequence 2, Appli
3	722	100.0	130	3	US-09-943-388-5	Sequence 5, Appli
4	722	100.0	130	3	US-09-927-876-81	Sequence 81, Appli
5	722	100.0	130	4	US-10-196-437A-5	Sequence 5, Appli
6	722	100.0	130	4	US-10-168-048A-1	Sequence 1, Appli
7	722	100.0	130	4	US-10-203-708-27	Sequence 27, Appli
8	722	100.0	130	4	US-10-449-140-1	Sequence 1, Appli
9	722	100.0	130	4	US-10-373-617A-9	Sequence 9, Appli
10	722	100.0	130	4	US-10-360-149-81	Sequence 81, Appli
11	722	100.0	130	4	US-10-457-047-81	Sequence 81, Appli

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:16:57 ; Search time 14.322 Seconds
(without alignments)
207.367 Million cell updates/sec

Title: US-10-733-597-2
Perfect score: 722
Sequence: 1 MKLAFLFLGPMALLLLAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	164	22.7	129	7	US-11-183-218-14	Sequence 14, Appl
2	155	21.5	165	6	US-10-915-763A-14	Sequence 14, Appl
3	155	21.5	165	7	US-11-183-218-72	Sequence 72, Appl
4	143	19.8	145	7	US-11-273-478-2	Sequence 2, Appl
5	92	12.7	38	7	US-11-243-438-24	Sequence 24, Appl
6	82	11.4	348	6	US-10-449-902-34800	Sequence 34800, A
7	78.5	10.9	469	7	US-11-246-999-41	Sequence 41, Appl
8	78.5	10.9	494	7	US-11-246-999-30	Sequence 30, Appl
9	78.5	10.9	567	7	US-11-246-999-50	Sequence 50, Appl

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:08:22 ; Search time 26.9915 Seconds
(without alignments)
463.411 Million cell updates/sec

Title: US-10-733-597-2
Perfect score: 722
Sequence: 1 MKLAFLFLGPMALLLLAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
<hr/>							
1	210	29.1	141	1	UTBOB		lutropin beta chai
2	209	28.9	144	1	UTCAB		gonadotropin beta
3	207	28.7	141	1	B60626		gonadotropin beta
4	207	28.7	146	1	S16763		gonadotropin beta
5	204.5	28.3	141	1	UTSHB		lutropin beta chai
6	201.5	27.9	140	2	A48166		gonadotropin II be
7	201	27.8	142	1	C36179		gonadotropin II be
8	199	27.6	136	2	I50554		gonadotropin II be
9	198	27.4	113	1	S07092		gonadotropin beta
10	192	26.6	142	2	I51232		gonadotropin II be
11	189	26.2	112	2	S21196		lutropin beta chai
12	189	26.2	147	2	I50994		gonadotropin II be
13	186.5	25.8	142	2	I50143		gonadotropin II be

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:03:21 ; Search time 212.627 Seconds
(without alignments)
565.554 Million cell updates/sec

Title: US-10-733-597-2

Perfect score: 722

Sequence: 1 MKLAFLFLGPMALLLLAGYG. VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	722	100.0	130	1	GPHB5_HUMAN	Q86yw7 homo sapien
2	636	88.1	130	1	GPHB5_MOUSE	Q812b2 mus musculu
3	619.5	85.8	129	2	Q5VJF5_RAT	Q5vjf5 rattus norv
4	590	81.7	115	2	Q2NL39_MOUSE	Q2nl39 mus musculu
5	440	60.9	99	2	Q4S6H4_TETNG	Q4s6h4 tetraodon n
6	428	59.3	124	2	Q4S0U3_TETNG	Q4s0u3 tetraodon n
7	213.5	29.6	149	1	GTHB2_CLUPA	Q9ygh2 clupea pall
8	211	29.2	128	2	Q5YFS0_ACIGU	Q5yfs0 acipenser g
9	211	29.2	128	2	Q9I997_ACIBE	Q9i997 acipenser b
10	210	29.1	140	2	Q5UK78_BRARE	Q5uk78 brachydanio
11	210	29.1	140	2	Q6TCF5_BRARE	Q6tcf5 brachydanio
12	210	29.1	141	1	LSHB_BOVIN	P04651 bos taurus
13	209	28.9	140	1	GTHB2_CARAU	Q98849 carassius a
14	209	28.9	144	1	GTHB2_CYPICA	P01235 cyprinus ca
15	208	28.8	122	2	Q306L6_9TELE	Q306l6 pimephales

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:22:24 ; Search time 83 Seconds
(without alignments)
583.915 Million cell updates/sec

Title: US-10-733-597-9

Perfect score: 600

Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	600	100.0	106	4	AAG64065		Aag64065 Human ant
2	600	100.0	106	5	AAU96154		Aau96154 Human mat
3	600	100.0	106	6	ABP72423		Abp72423 Human gly
4	600	100.0	106	8	ADF72484		Adf72484 Mature hu
5	600	100.0	106	9	ADW86161		Adw86161 Human Zlu
6	600	100.0	106	9	AEC83182		Aec83182 Human mat
7	600	100.0	129	5	AAU96157		Aau96157 Human BRP

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:14:53 ; Search time 32.339 Seconds
(without alignments)
286.906 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	521	86.8	118	3	US-10-162-335-26	Sequence 26, Appl
2	178	29.7	149	1	US-08-425-673-5	Sequence 5, Appl
3	170	28.3	104	2	US-08-918-288-74	Sequence 74, Appl
4	170	28.3	104	2	US-09-282-357-74	Sequence 74, Appl
5	170	28.3	108	2	US-08-918-288-73	Sequence 73, Appl
6	170	28.3	108	2	US-09-282-357-73	Sequence 73, Appl
7	170	28.3	111	2	US-08-918-288-72	Sequence 72, Appl
8	170	28.3	111	2	US-09-282-357-72	Sequence 72, Appl
9	164	27.3	97	2	US-10-099-322-299	Sequence 299, App
10	164	27.3	97	2	US-10-044-564-299	Sequence 299, App

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:23:34 ; Search time 67 Seconds
(without alignments)
732.847 Million cell updates/sec

Title: US-10-733-597-9

Perfect score: 600

Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 500 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	600	100.0	106	3	US-09-818-954A-3	Sequence 3, Appli
2	600	100.0	106	3	US-09-943-388-9	Sequence 9, Appli
3	600	100.0	106	3	US-09-927-876-83	Sequence 83, Appli
4	600	100.0	106	4	US-10-196-437A-6	Sequence 6, Appli
5	600	100.0	106	4	US-10-168-048A-5	Sequence 5, Appli
6	600	100.0	106	4	US-10-449-140-3	Sequence 3, Appli
7	600	100.0	106	4	US-10-360-149-83	Sequence 83, Appli
8	600	100.0	106	4	US-10-457-047-83	Sequence 83, Appli
9	600	100.0	106	4	US-10-459-000A-6	Sequence 6, Appli
10	600	100.0	106	5	US-10-733-597-9	Sequence 9, Appli
11	600	100.0	106	5	US-10-811-081-83	Sequence 83, Appli

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:16:57 ; Search time 11.678 Seconds
(without alignments)
207.367 Million cell updates/sec

Title: US-10-733-597-9

Perfect score: 600

Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	164	27.3	129	7	US-11-183-218-14	Sequence 14, Appl
2	143	23.8	145	7	US-11-273-478-2	Sequence 2, Appl
3	143	23.8	165	6	US-10-915-763A-14	Sequence 14, Appl
4	143	23.8	165	7	US-11-183-218-72	Sequence 72, Appl
5	92	15.3	38	7	US-11-243-438-24	Sequence 24, Appl
6	82	13.7	348	6	US-10-449-902-34800	Sequence 34800, A
7	76.5	12.8	257	6	US-10-449-902-36378	Sequence 36378, A
8	71.5	11.9	376	6	US-10-449-902-53472	Sequence 53472, A
9	65	10.8	368	6	US-10-449-902-30253	Sequence 30253, A

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:08:22 ; Search time 22.0085 Seconds
(without alignments)
463.411 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	% No. Score Match Length DB ID					Description
		Score	Match	Length	DB	ID	
1	209	34.8	144	1	UTCAB		gonadotropin beta
2	207	34.5	141	1	B60626		gonadotropin beta
3	207	34.5	146	1	S16763		gonadotropin beta
4	201	33.5	141	1	UTBOB		lutropin beta chai
5	201	33.5	141	1	UTSHB		lutropin beta chai
6	199	33.2	136	2	I50554		gonadotropin II be
7	199	33.2	140	2	A48166		gonadotropin II be
8	199	33.2	142	1	C36179		gonadotropin II be
9	198	33.0	113	1	S07092		gonadotropin beta
10	191	31.8	142	2	I51232		gonadotropin II be
11	189	31.5	112	2	S21196		lutropin beta chai
12	189	31.5	147	2	I50994		gonadotropin II be
13	186	31.0	142	2	I50143		gonadotropin II be

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:03:21 ; Search time 173.373 Seconds
(without alignments)
565.554 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	600	100.0	130	1	GPHB5_HUMAN	Q86yw7 homo sapien
2	577	96.2	115	2	Q2NL39_MOUSE	Q2nl39 mus musculu
3	577	96.2	130	1	GPHB5_MOUSE	Q812b2 mus musculu
4	576	96.0	129	2	Q5VJF5_RAT	Q5vjf5 rattus norv
5	440	73.3	99	2	Q4S6H4_TETNG	Q4s6h4 tetraodon n
6	409	68.2	124	2	Q4S0U3_TETNG	Q4s0u3 tetraodon n
7	211	35.2	128	2	Q5YFS0_ACIGU	Q5yfs0 acipenser g
8	211	35.2	128	2	Q9I997_ACIBE	Q9i997 acipenser b
9	209	34.8	140	1	GTHB2_CARAU	Q98849 carassius a
10	209	34.8	144	1	GTHB2_CYPCA	P01235 cyprinus ca
11	208	34.7	122	2	Q306L6_9TELE	Q30616 pimephales
12	208	34.7	128	2	Q6PV99_ACISC	Q6pv99 acipenser s
13	207	34.5	140	2	Q98TY3_MYLPI	Q98ty3 mylopharyng
14	207	34.5	141	1	GTHB2_HYPMO	P37038 hypophthalm
15	207	34.5	146	1	GTHB2_CTEID	P30984 ctenopharyn